



VERIFICATION OF TRANSLATION

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[Title of the Invention] GLUCOSE DEHYDROGENASE β SUBUNIT AND
DNA ENCODING THE SAME

[Claims]

[Claim 1] protein defined in the following (A) or
(B):

(A) a protein which has at least the amino acid
sequence comprising amino acids 23 to 425 of SEQ ID NO: 16;

(B) a protein which has at least the amino acid
sequence comprising amino acids 23 to 425 of SEQ ID NO: 16
including substitution, deletion, insertion or addition of 1
to 20 amino acid residues.

[Claim 2] A DNA encoding a protein defined in the
following (A) or (B):

(A) a protein which has at least the amino acid
sequence comprising amino acids 23 to 425 of SEQ ID NO: 16;

(B) a protein which has at least the amino acid
sequence comprising amino acids 23 to 425 of SEQ ID NO: 16
including substitution, deletion, insertion or addition of 1
to 20 amino acid residues.

[Claim 3] The DNA according to claim 2, wherein the
DNA is defined in the following (a) or (b):

(a) a DNA comprising the nucleotide sequence
consisting of nucleotides 187 to 1398 of SEQ ID NO: 15;

(b) a DNA which is hybridizable with the nucleotide
sequence consisting of nucleotides 187 to 1398 of SEQ ID NO:
15 under stringent conditions.

[Claim 4] The DNA according to claim 3, further
comprising the nucleotide sequence consisting of nucleotides
121 to 187 of SEQ ID NO: 15.

[Claim 5] A recombinant vector comprising the DNA according to any one of claims 2 to 4.

[Claim 6] A transformant transformed with the DNA according to any one of claims 2 to 4 or the recombinant vector according to claim 5.

[Claim 7] A method of producing a glucose dehydrogenase β subunit, comprising culturing the transformant according to claim 6 to produce a glucose dehydrogenase β subunit as an expression product of the DNA, and collecting the produced β subunit.

[Claim 8] The DNA according to claim 3 or 4, further comprising the nucleotide sequence encoding an α subunit and a γ subunit of glucose dehydrogenase of *Burkholderia cepacia*.

[Claim 9] A recombinant vector comprising the DNA according to claim 8.

[Claim 10] A transformant transformed with the DNA according to claim 8 or the recombinant vector according to claim 9.

[Claim 11] A method of producing a glucose dehydrogenase complex, comprising culturing the transformant according to claim 10 to produce a glucose dehydrogenase complex as an expression product of the DNA, and collecting the produced complex.

[Detailed Description of the Invention]

[Field of Industrial Application]

The present invention relates to cytochrome C that constitutes a glucose dehydrogenase β subunit, to a DNA encoding the cytochrome C, and to their utilization. The glucose dehydrogenase is useful for a glucose sensor using an enzyme electrode or the like.

[Prior Art]

Biosensors using an enzyme that specifically reacts with a particular substrate are being actively developed in various industrial fields. As for a glucose sensor, which is one of the biosensors, in particular, measurement methods and devices utilizing such methods are being actively developed mainly in medical fields. For example, the glucose sensor has a history of about 40 years since Clark and Lyons first reported about a biosensor including glucose oxidase and an oxygen electrode in combination in 1962 (L.c. Clark, J. and Lyons, C. "Electrode systems for continuous monitoring in cardiovascular surgery." Ann. n. y. Acad. Sci., 105: 20-45).

Thus, the adoption of glucose oxidase as an enzyme for the glucose sensor has a long history. This is because glucose oxidase shows high substrate specificity for glucose and superior thermal stability, this enzyme can further be produced in a large scale, and its production cost is lower than those of other enzymes. The high substrate specificity means that this enzyme does not react with a saccharide other than glucose, and this leads to an advantage that accurate measurement can be achieved without error in measurement values. Further, the superior thermal stability means that problems concerning denaturation of the enzyme and inactivation of its enzymatic activity due to heat can be prevented, and this leads to an advantage that accurate measurement can be performed over a long period of time.

However, although glucose oxidase has advantages as described above, it has a problem that the enzyme is affected by dissolved oxygen and this affects measurement

results.

Meanwhile, in addition to glucose oxidase, a glucose sensor utilizing glucose dehydrogenase (hereinafter referred to as "glucose dehydrogenase" or "GDH") has also been developed. This enzyme is also found in microorganisms. For example, there are known glucose dehydrogenase derived from *Bacillus* (EC 1.1.1.47) and glucose dehydrogenase derived from *Cryptococcus* (EC 1.1.1.119).

The former glucose dehydrogenase (EC 1.1.1.47) is an enzyme that catalyzes a reaction of β -D-glucose + $\text{NAD(P)}^+ \rightarrow$ D- δ -gluconolactone + $\text{NAD(P)H} + \text{H}^+$, and the latter glucose dehydrogenase (EC 1.1.1.119) is an enzyme that catalyzes a reaction of D-glucose + $\text{NADP}^+ \rightarrow$ D- δ -gluconolactone + $\text{NADPH} + \text{H}^+$. The aforementioned glucose dehydrogenases derived from microorganisms are already marketed.

These glucose dehydrogenases have an advantage that they are not affected by dissolved oxygen in a measurement sample. This leads to an advantage that accurate measurement can be achieved without causing errors in measurement results even when the measurement is performed in an environment in which the oxygen partial pressure is low, or a high-concentration sample requiring a large amount of oxygen is used for the measurement.

However, although conventional glucose dehydrogenase is not affected by dissolved oxygen, it has problems of poor thermal stability and substrate specificity poorer than that of glucose oxidase. For an enzyme which is used in a sensor, an enzyme that overcomes disadvantages of both of glucose oxidase and glucose dehydrogenase has been desired.

The inventors of the present invention reported

results of their studies about GDH using samples collected from soil near hot springs in Sode, K., Tsugawa, W., Yamazaki, T., Watanabe, M., Ogasawara, N., and Tanaka, M., Enzyme Microb. Technol., 19, 82-85 (1996); Yamazaki, T., Tsugawa, W. and Sode, K., Appli. Biochemi. and Biotec., 77-79/0325 (1999); and Yamazaki, T., Tsugawa, W. and Sode, K., Biotec. Lett., 21, 199-202 (1999). The microorganisms in those samples produce a coenzyme-binding GDH, and the enzymologic properties such as optimum reaction temperature, thermal stability, and substrate specificity have already been clear (See the aforementioned documents). This enzyme is a hetero oligomeric enzyme that is constituted by a catalyst subunit having a high thermal resistance (α subunit), an electron transferring subunit (β subunit), and γ subunit having an unknown function, and the activity peaks thereof are observed at 45°C and 75°C, respectively. Further, the γ and α subunit genes have been cloned, and it has been clarified that the aforementioned microorganism belongs to *Burkholderia cepacia*, and the N-terminal amino acid sequence of the β subunit has been clarified (Ken Inose, Tokyo Agricultural Engineering University Master's Thesis (2001)). However, the structure of the β subunit gene has not been reported.

[Problem to be solved by the invention]

An object of the present invention is to provide a DNA encoding a GDH β subunit of a microorganism belonging to the genus *Burkholderia* and a method of using the DNA.

[Means to Solve the Problem]

The inventors of the present invention have further advanced the study on GDH of *Burkholderia cepacia* KS1 strain

and were successful in isolating a DNA encoding a GDH β subunit, thereby completing the present invention.

That is, the present invention can be described as follows.

(1) A protein defined in the following (A) or (B):

(A) a protein which has at least the amino acid sequence comprising amino acids 23 to 425 of SEQ ID NO: 16;

(B) a protein which has at least the amino acid sequence comprising amino acids 23 to 425 of SEQ ID NO: 16 including substitution, deletion, insertion or addition of 1 to 20 amino acid residues.

(2) A DNA encoding a protein defined in the following (A) or (B):

(A) a protein which has at least the amino acid sequence consisting of amino acids 23 to 425 of SEQ ID NO: 16;

(B) a protein which has at least the amino acid sequence comprising amino acids 23 to 425 of SEQ ID NO: 16 including substitution, deletion, insertion or addition of 1 to 20 amino acid residues.

(3) The DNA according to item (2), in which the DNA is defined in the following (a) or (b):

(a) a DNA including the nucleotide sequence consisting of nucleotides 187 to 1398 of SEQ ID NO: 15;

(b) a DNA which is hybridizable with the nucleotide sequence consisting of nucleotides 187 to 1398 of SEQ ID NO: 15 under stringent conditions.

(4) The DNA according to item (3), further including the nucleotide sequence consisting of nucleotides 121 to 187 of SEQ ID NO: 15.

(5) A recombinant vector including a DNA according to any one of items (2) to (4).

(6) A transformant transformed with a DNA according to any one of items (2) to (4) or the recombinant vector according to item (5).

(7) A method of producing a glucose dehydrogenase β subunit, including culturing the transformant according to item (6) to produce a glucose dehydrogenase β subunit as an expression product of the DNA, and collecting the produced β subunit.

(8) The DNA according to item (3) or (4), further including the nucleotide sequence encoding an α subunit and a γ subunit of glucose dehydrogenase of *Burkholderia cepacia*.

(9) A recombinant vector including the DNA according to item (8).

(10) A transformant transformed with the DNA according to item (8) or the recombinant vector according to item (9).

(11) A method of producing a glucose dehydrogenase complex, including culturing the transformant according to item (10) to produce a glucose dehydrogenase complex as an expression product of the DNA, and collecting the produced complex.

[Embodiment of the Invention]

Hereinafter, the present invention will be described in detail.

The inventors of the present invention have searched and isolated a DNA encoding a GDH β subunit of *Burkholderia cepacia* KS1 strain. The aforementioned strain was deposited at International Patent Organism Depositary, National Institute of Advanced Industrial Science and Technology (Central 6, 1-1-1, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken,

Japan, postal code: 305-8566) and received a microorganism accession number of FERM BP-7306. In the present specification, the DNA encoding the GDH β subunit is sometimes referred to as the DNA of the present invention, " β subunit structural gene", or simply " β subunit gene".

The inventors of the present invention have confirmed that GDH produced by *Burkholderia cepacia* KS1 strain is a polymeric protein containing an α subunit, a β subunit, and a γ subunit. The protein of the present invention corresponds to the β subunit out of these subunits. Spectrophotometric analyses for GDH indicate that the absorption wavelength of an oxidized GDH resembles the absorption wavelengths of alcohol dehydrogenase and aldehyde dehydrogenase of *Gluconobacter* sp. and *Acetobacter* sp. that are composed of dehydrogenase cytochrome complex, and this absorption is lost by heat treatment. This fact and the difference in optimum reaction temperature of the GDH between presence and absence of the β subunit as described below have suggested that the β subunit is composed of cytochrome C.

Physical and chemical properties of the above GDH are shown below.

- (1) Function: the enzyme catalyzes dehydrogenation reaction of glucose.
- (2) The enzyme consists of subunits showing a molecular weight of about 60 kDa and a molecular weight of about 43 kDa in SDS-polyacrylamide gel electrophoresis under a reducing condition.
- (3) The enzyme shows a molecular weight of about 380 kDa in gel filtration chromatography using TSK Gel G3000SW

(Manufactured by Tosoh Corporation).

(4) Optimal reaction temperature: around 45°C (Tris-HCl buffer, pH 8.0).

Physical and chemical properties of an α -subunit alone are shown below.

(1)' The protein has a glucose dehydrogenase activity.

(2)' The protein shows a molecular weight of about 60 kDa in SDS-polyacrylamide gel electrophoresis under a reducing condition.

(3)' Optimal reaction temperature: around 75°C (Tris-HCl buffer, pH 8.0).

The β subunit can be obtained together with other subunits from a culture of *Burkholderia cepacia* KS1 strain by purifying a GDH complex using GDH activity as an index. The GDH activity can be measured in the same manner as in the known GDH activity measurement. Specifically, the measurement can be performed as follows. A 10 mM potassium phosphate buffer (pH 7.0) containing 594 μ M 1-methoxyphenazine methosulfate (mPMS) and 5.94 μ M 2,6-dichlorophenol indophenol (DCIP) are added to an enzyme sample and glucose as a substrate, and the mixture is incubated at 37°C. A change in the absorbance of DCIP at 600 nm is traced using a spectrophotometer, and the decrease rate in the absorbance is defined as an enzyme reaction rate.

In addition, since the nucleotide sequence of a gene encoding the β subunit (SEQ ID NO: 15) has been determined by the present invention, the β subunit can also be produced by expressing a DNA having the nucleotide sequence or a DNA encoding the same amino acid sequence as the amino acid sequence encoded by this DNA in a suitable host. The amino

acid sequence that can be encoded by the open reading frame (ORF) of SEQ ID NO: 15 is shown in SEQ ID NO: 16. The N-terminal amino acid sequence of the β subunit determined from the protein was identical to the amino acids 23 to 38 of SEQ ID NO: 16. Therefore, the amino acids 1 to 22 are presumed to be a signal peptide. Note that although amino acid residue 1 is described as Val in SEQ ID NOs: 15 and 16, it has a high possibility to be Met and it also has a possibility to be dropped after the translation.

Results of homology search on the aforementioned amino acid sequence by BLAST indicated overall high homologies; 65% homology with a cytochrome C subunit of oxidoreductase dehydrogenase derived from *Ralstonia solanacearum*, 48% homology with a cytochrome C subunit of sorbitol dehydrogenase derived from *Gluconobacter oxydans*, 44% homology with a cytochrome C subunit of gluconic acid dehydrogenase derived from *Eriwinia cypripedii*, and 55.7% homology on the nucleotide sequence level or a 46.4% homology on the amino acid level with a cytochrome C subunit of 2-keto-gluconic acid dehydrogenase derived from *Pantoea citrea*. Furthermore, the amino acid sequences of these cytochromes C reserved a hem-linking motif (SEQ ID NO: 18). These facts show that the β subunit of the present invention is cytochrome C.

The β subunit of the present invention may be a protein having the amino acid sequence consisting of the amino acids 23 to 425 of SEQ ID NO: 16 including substitution, deletion, insertion, or addition of 1 to 20, preferably 1 to 10, more preferably 1 to 5 amino acid residues in the amino acid sequence so long as it can function as a GDH β subunit. Note

that the term "functions as a GDH β subunit" means "functions as cytochrome C without deteriorating the enzyme activity of the GDH".

The DNA of the present invention is a DNA that encodes the aforementioned β subunit and can be obtained from, for example, *Burkholderia cepacia* KS1 strain. The DNA of the present invention has been isolated from the chromosomal DNA of *Burkholderia cepacia* KS1 strain in the course of completion of the present invention. The DNA of the present invention can be obtained, for example, by PCR using primers having nucleotide sequences of SEQ ID NOs: 13 and 14 and the chromosomal DNA of *Burkholderia cepacia* KS1 strain as a template. In addition, since the nucleotide sequence of the DNA of the present invention and the amino acid sequence encoded by the nucleotide sequence have been clarified by the present invention, the DNA of the present invention can also be obtained by performing chemical synthesis based on these sequences. Furthermore, the DNA of the present invention can be obtained from the chromosomal DNA of *Burkholderia cepacia* KS1 strain by hybridization using the oligonucleotide prepared based on the aforementioned sequences as probes. Similarly, variants can be obtained from strains other than *Burkholderia cepacia*.

The DNA of the present invention may be one encoding a protein having the amino acid sequence consisting of the amino acids 23 to 425 of SEQ ID NO: 16 or one having the amino acid sequence including substitution, deletion, insertion, or addition of 1 to 20, preferably 1 to 10, more preferably 1 to 5 amino acid residues and encoding a protein that functions as a GDH β subunit.

Specifically, the DNA of the present invention includes a DNA having the nucleotide sequence consisting of the nucleotides 187 to 1398 of SEQ ID NO: 15. Further, the DNA of the present invention may be a DNA that hybridizes with SEQ ID NO: 15 or a probe that can be prepared from this sequence under stringent conditions and encodes a protein that can function as a β subunit. The stringent conditions include those conditions whereby DNAs having a 70% or more, preferably 80% or more, more preferably 90% or more homology to each other hybridize, specifically conditions of 1 \times SSC, 0.1% SDS, and 60°C.

The GDH β subunit can be produced by culturing a transformant that harbors the DNA of the present invention or a recombinant vector containing the DNA of the present invention to produce the GDH β subunit as an expression product of the DNA, and by collecting the GDH β subunit from the microorganism cells or the culture medium. In this case, the DNA encoding the GDH β subunit of the present invention may be expressed together with a DNA encoding an α subunit or further a DNA encoding a γ subunit to produce a GDH complex. A DNA fragment that sequentially encodes the γ subunit and the α subunit can be obtained by PCR using primers having nucleotide sequences of SEQ ID NOs: 18 and 19.

Examples of the microorganism that produces the GDH β subunit or the GDH complex include: enterobacteria including *Escherichia coli*; Gram negative bacteria such as *Pseudomonas* and *Gluconobacter*; Gram positive bacteria including bacteria belonging to the genus *Bacillus* such as *Bacillus subtilis*; yeasts such as *Saccharomyces cerevisiae*; and molds such as *Aspergillus niger*. However, the microorganism is not limited

to these and any microorganism may be used so long as it is a host microorganism suitable for the production of foreign proteins.

Vectors that are used for cloning or expressing the DNA of the present invention are suitably those constructed for gene recombination from plasmids or phages that can autonomously replicate in host microorganisms. Examples of vectors for *E. coli* include pBR322, pUC18, pUC118, pUC19, pUC119, pTrc99A, pBluescript, or SuperCosI, which is a cosmid. Transfer of the DNA from the vector that has been used in cloning the DNA of the present invention to other recombinant vectors suitable for expression, etc. can be readily performed by recovering the DNA of the present invention from a recombinant vector containing the DNA of the present invention with a restriction enzyme or by the PCR method and ligating it with a vector fragment. Furthermore, transformation of microorganisms with these vectors can be performed by the competent cell method by treatment with calcium for bacteria belonging to the genus *Escherichia*, the protoplast method for bacteria belonging to the genus *Bacillus*, the KU method or the KUR method for yeasts, and the micromanipulation method for molds and so forth. In addition, the electroporation method can also be used widely.

Selection of host microorganisms based on presence or absence of introduction of the target recombinant vector therein may be performed by using a chemical resistance marker of the vector containing the target DNA and the like. For example, a microorganism that can grow in a selective medium based on a chemical resistance marker and produces

GDH may be selected.

As for the culture method of the transformant, culture conditions may be selected by considering nutritional and physiological properties of the host. In many cases, liquid culture is performed. It is industrially advantageous to perform aeration culture with shaking.

As nutrients of the medium, those usually used for culture of microorganisms may be widely used. As carbon sources, any assimilable carbon compounds may be used, and examples of the compounds to be used include glucose, sucrose, lactose, maltose, lactose, molasses, pyruvic acid and so forth. Furthermore, as nitrogen sources, any utilizable nitrogen compounds may be used, and examples of the compounds to be used include peptone, meat extracts, yeast extracts, casein hydrolysates, soybean cake alkaline extracts and so forth. In addition, phosphate, carbonate, sulfate, salts of magnesium, calcium, potassium, iron, manganese, zinc and so forth, particular amino acids, particular vitamins and so forth are used as required.

Although the culture temperature can be appropriately changed in a range in which a bacteria grows and produces the protein of the present invention, it is preferably about 20°C to 42°C. The culture time somewhat varies depending on the conditions. However, the culture may be completed at an appropriate time estimated to give the maximum GDH yield, and the culture time is usually about 12 to 72 hours. Although pH of the medium may be appropriately changed in a range in which a bacteria grows and produces the protein of the present invention, it is preferably in the range of about pH 6.0 to 9.0.

The culture medium containing cells of the microorganism producing the protein of the present invention in the culture can be collected and utilized as they are. However, when the protein of the present invention exists in the culture medium, the culture medium is usually separated into the solution containing the protein of the present invention and microorganism cells by filtration, centrifugation or the like in a conventional manner and then used. When the protein of the present invention exists in the cells, the cells are collected from the obtained culture by means of filtration, centrifugation or the like, and then disrupted by a mechanical method or an enzymatic method such as use of lysozyme. Further, a chelating agent such as EDTA and a surfactant are added to the cell to solubilize the protein of the present invention, as required, followed by isolation and collection as an aqueous solution.

Protein may be precipitated from the thus-obtained protein-containing solution by, for example, vacuum concentration, membrane concentration, salting out with ammonium sulfate, sodium sulfate or the like, or a fractional precipitation with a hydrophilic organic solvent such as methanol, ethanol, and acetone. Further, heat treatment and isoelectric point treatment are also effective purification means. Then, purification can be performed by a suitable combination of gel filtration using an adsorbent, gel filtration agent, etc., absorption chromatography, ion exchange chromatography and affinity chromatography to obtain a purified protein of the present invention.

A purified enzyme preparation can be obtained by isolation and purification based on column chromatography.

Although the purified enzyme preparation is preferably purified to such an extent that a single band is obtained in electrophoresis (SDS-PAGE), it may contain an α -subunit or a γ -subunit.

The thus-obtained purified enzyme can be powdered by, for example, lyophilization, vacuum drying, spray drying or the like and distributed.

The GDH complex consisting of a β -subunit, an α -subunit, or whenever required, a γ -subunit of the present invention, or transformants containing those, may be used for an enzyme electrode of a glucose sensor. As the electrode, a carbon electrode, gold electrode, platinum electrode or the like may be used, and the GDH of the present invention is immobilized on the electrode. Examples of the method for immobilization include a method of using a crosslinking reagent, a method of entrapping the enzyme in a polymer matrix, a method of covering the enzyme with a dialysis membrane, methods of using a photocrosslinking polymer, conductive polymer, oxidation-reduction polymer or the like. Alternatively, the enzyme may be immobilized in a polymer or immobilized on an electrode by adsorption together with an electronic mediator of which typical examples are ferrocene and derivatives thereof, or these methods may be used in combination. Typically, the glucose dehydrogenase of the present invention is immobilized on a carbon electrode by using glutaraldehyde, and then glutaraldehyde is blocked by a treatment with a reagent having an amine group.

The glucose concentration can be measured as follows. A buffer is placed in a thermostatic cell, and a mediator is

added thereto. Then, a constant temperature is maintained. As the mediator, potassium ferricyanide, phenazine methosulfate and so forth may be used. An electrode on which the enzyme of the present invention is immobilized is used as a working electrode, and a counter electrode (e.g., platinum electrode) and a reference electrode (e.g., Ag/AgCl electrode) are used. After a constant voltage is applied to the carbon electrode to obtain a steady-state current, a sample containing glucose is added thereto and the increase of the current is measured. The glucose concentration in the sample can be calculated according to a calibration curve produced by using glucose solutions having standard concentrations.

The GDH complex containing the β subunit of the present invention may be used as a component in an assay kit for saccharides such as glucose. Typically, the kit includes in addition to the GDH complex, a buffer necessary for the assay, a mediator, a standard solution of, for example, glucose for preparing a calibration curve, and a manual on the use of the kit. The enzyme according to the present invention may be provided in various forms, for example, as a freeze-dried reagent or as a solution in a suitable stock solution.

[Examples]

Hereinafter, the present invention will be described specifically with reference to examples.

[Reference Example 1] Isolation of a gene encoding GDH α subunit of *Burkholderia cepacia* KS1 strain

<1> Preparation of chromosomal DNA from *Burkholderia cepacia*

KS1 strain.

A chromosomal gene was prepared from the *Burkholderia cepacia* KS1 strain in a conventional manner. That is, the bacterial strain was shaken overnight at 34°C by using a TL liquid medium (10 g of polypeptone, 1 g of yeast extract, 5 g of NaCl, 2 g of KH₂PO₄, 5 g of glucose in 1 L, pH 7.2). The grown cells were collected by centrifugation. The cells were suspended in a solution containing 10 mM NaCl, 20 mM Tris-HCl (pH 8.0), 1 mM EDTA, 0.5% SDS, and 100 µg/ml proteinase K and treated at 50°C for 6 hours. This mixture was added to an equivalent volume of phenol-chloroform and stirred at room temperature for 10 minutes, and then the supernatant was collected by centrifugation. The supernatant was added to sodium acetate to give a final concentration of 0.3 M and overlaid with two-fold volume of ethanol to precipitate chromosomal DNA in the intermediate layer. The DNA was taken up with a glass rod, washed with 70% ethanol, and dissolved in an appropriate amount of TE buffer to obtain a chromosomal DNA solution.

<2> Determination of N-terminus amino acid sequence of GDH α -subunit

GDH purified in the same manner as in Example 2 was concentrated by lyophilization and separated by SDS-electrophoresis using 12.5% polyacrylamide to isolate the α -subunit. The thus obtained α -subunit was transferred onto a polyvinylidene fluoride membrane, and then the N-terminus amino acid sequence was determined by using an amino acid sequencer (PPSQ-10, manufactured by Shimadzu Corporation). As a result, it was found that the enzyme contained a peptide sequence consisting of 11 residues of the amino acid

numbers 2 to 12 in the amino acid sequence of SEQ ID NO: 3.

<3> Cloning of a gene encoding α -subunit

The DNA prepared in <1> (1 μ g) was subjected to partial digestion with a restriction enzyme *Sau3AI*, followed by treatment with calf intestinal alkaline phosphatase (CIAP). Separately, SuperCosI (obtained from Stratagene), which is a cosmid, was treated with *Bam*HI, and the DNA fragment obtained by the partial digestion of the chromosomal DNA fragment derived from the α -15 strain with *Sau3AI* was introduced into SuperCosI by using T4 DNA ligase. *E. coli* XL-1 Blue MR (obtained from Stratagene) was transformed with the obtained recombinant DNA. A transformant was selected on an LB agar medium containing 10 μ g/ml neomycin and 25 μ g/ml ampicillin based on neomycin resistance and ampicillin resistance, which are antibiotic resistances on SuperCosI. The obtained transformant was cultured in the LB liquid medium. These transformant cells were collected and suspended in a reagent for measuring the GDH activity, and a clone was selected by using dehydrogenase activity for glucose as an index. As a result, one clone showing the glucose dehydrogenase activity was obtained.

<4> Subcloning

DNA fragments containing the target gene were prepared from the cosmid, SuperCosI, containing the gene encoding the α -subunit obtained in <3>. The inserted gene fragments were cleaved from the cosmid by using a restriction enzyme *Not*I. These DNA fragments were treated with a restriction enzyme *Xba*I and introduced into a plasmid pUC18 digested with *Xba*I. The *E. coli* DH5 α -MCR strain was transformed with the

plasmid pUC18 containing each inserted fragment, and colonies appeared on an LB agar medium containing 50 µg/ml of ampicillin were collected. The obtained transformants were cultured in the liquid LB medium, followed by examination for the GDH activity in the cells in the same manner as in <3>. As a result, a transformant showing the GDH activity was obtained. The plasmid was extracted from this transformant, and the inserted DNA fragment was analyzed. As a result, an insert of about 8.8 kbp was confirmed. This plasmid was designated as pKS1.

<5> Determination of the nucleotide sequence

Restriction enzyme analysis of the inserted DNA fragment in pKS1 was performed and the nucleotide sequence of the fragment was determined according to the conventional method. As a result, the sequence of the DNA encoding the N-terminus amino acid sequence of the α -subunit found in <2> was confirmed in this inserted DNA fragment, and an open reading frame containing this sequence was found. The determined nucleotide sequence and the amino acid sequence that can be encoded by this nucleotide sequence are as shown in SEQ ID NOs: 1 and 3. In the nucleotide sequence of SEQ NO: 1, nucleotide sequence downstream from nucleotide number 2,386 encode amino acid sequence of SEQ NO: 4, and encode β -subunit.

[Reference Example 2] Production of a GDH- α -subunit by recombinant *E. coli*.

Since the nucleotide sequence of the α -subunit was determined, a vector was prepared using the aforementioned structural gene of the α -subunit, and a transformant was further produced using this vector.

First, a gene to be inserted into the vector was prepared as follows.

Amplification was performed by PCR using a genome fragment derived from the KS1 strain as a template so that a desired restriction enzyme site is included. The following pair of oligonucleotide primers were used in PCR.

(Forward)

5'-CCCAAGCTTGGGCCGATACCGATACGCA-3' (SEQ ID NO: 5)

(Reverse)

5'-GAGAAGCTTTCCGCACGGTCAGACTTCC-3' (SEQ ID NO: 6)

The gene amplified by PCR was digested with a restriction enzyme *HindIII* and inserted into an expression vector pFLAG-CTS (SIGMA) at its cloning site, *HindIII* site. The obtained plasmid was designated as pFLAG-CTS/ α .

The *E. coli* DH5 α MCR strain was transformed with the aforementioned plasmid pFLAG-CTS/ α , and colonies appeared on the LB agar medium containing 50 μ g/ml of ampicillin were collected.

Further, when the open reading frame of the pKS1 inserted fragment was searched in the upstream of the α -subunit, a structural gene consisting of 507 nucleotides encoding a polypeptide including 168 amino acid residues shown in SEQ ID NO: 2 (nucleotide numbers 258 to 761 in SEQ ID NO: 1) was newly found. This structural gene was considered to encode the γ -subunit.

Since it was found that the region encoding the γ -subunit existed upstream of the coding region of the α -subunit, a recombinant vector containing a gene having a polycistronic structure continuously including the γ -subunit and the α -subunit was produced, and a transformant

introduced with this vector was constructed.

First, a gene to be inserted into the vector was prepared as follows.

Amplification was performed by PCR using a genome fragment derived from the KS1 strain continuously including the structural gene of the γ -subunit and the structural gene of the α -subunit as a template so that a desired restriction enzyme site is included. The following pair of oligonucleotide primers were used for PCR.

(Forward)

5'-CATGCCATGGCACACAACGACAACACT-3' (SEQ ID NO: 7)

(Reverse)

5'-CCCAAGCTTGGGTCAGACTTCCTTCTTCAGC-3' (SEQ ID NO: 8)

The 5'-terminus and the 3'-terminus of the gene amplified by PCR were digested with *Nco*I and *Hind*III, respectively, and the gene was inserted into the vector pTrc99A (Pharmacia) at its cloning site, *Nco*I/*Hind*III site. The obtained plasmid was named pTrc99A/ γ + α .

The *E. coli* DH5 α MCR strain was transformed with the aforementioned plasmid pTrc99A/ γ + α , and colonies appeared on the LB agar medium containing 50 μ g/ml of ampicillin were collected.

The α -subunit was produced using the *E. coli* DH5 α MCR strain transformed with each of the aforementioned plasmids pKS1, pFLAG-CTS/ α and pTrc99A/ γ + α . Each transformant was inoculated into 3 ml of the LB medium containing 50 μ g/ml of ampicillin and cultured at 37°C for 12 hours, and the cells were collected by centrifugation. The cells were disrupted by using a French press (1,500 kgf), and a membrane fraction (10 mM potassium phosphate buffer, pH 6.0) was isolated by

ultracentrifugation (4°C, 160,400 x g, 90 minutes).

[Reference Example 3] Confirmation of GDH activity

First, the GDH activity in each of the aforementioned membrane fractions was confirmed. Specifically, visual determination was performed by using 10 mM potassium phosphate buffer (pH 7.0) containing 594 μ M of methylphenazine methosulfate (mPMS) and 5.94 μ M of 2,6-dichlorophenolindopheol (DCIP). The results are shown below. The number of + represents the degree of color change from blue to colorless.

Membrane fraction of cultured transformant transformed with pFLAG-CTS/ α : +

Membrane fraction of cultured transformant transformed with pKS1 : ++

Membrane fraction of cultured transformant transformed with pTrc99A/ γ + α : +++

The GDH activity of the membrane fraction of the cultured transformant transformed with pFLAG-CTS/ α containing only with the α -subunit was the lowest, and the GDH activity of the membrane fraction of the cultured transformant transformed with pTrc99A/ γ + α , with which a vector was efficiently constructed, was the highest.

Although the α -subunit was expressed even in the transformant transformed with a vector using only the structural gene of the α -subunit, the α -subunit could be efficiently obtained by using a vector containing the structural gene of the γ -subunit and the structural gene of the α -subunit in combination.

Glucose was assayed using the glucose dehydrogenase of the present invention. The enzymatic activity of the glucose dehydrogenase (α -subunit) of the present invention was measured by using glucose having various concentrations. The GDH activity was measured in 10 mM potassium phosphate buffer (pH 7.0) containing 594 μ M of methylphenazine methosulfate (mPMS) and 5.94 μ M of 2,6-dichlorophenolindopheol (DCIP). An enzyme sample and glucose serving as a substrate were added thereto, followed by incubation at 37°C, and change in the absorbance of DCIP at 600nm was monitored by using a spectrophotometer. The decreasing rate of the absorbance was measured as an enzymatic reaction rate. Glucose could be quantified in the range of 0.01 to 1.0 mM using the GDH of the present invention.

[Example 1] Isolation of gene encoding a GDH β -subunit of *Burkholderia cepacia* KS1 strain

<1> Searching for *Burkholderia cepacia* KS1 strain GDH β subunit

GDH β subunit gene derived from KS1 strain was searched using *Burkholderia cepacia* J2315 strain genome database of Sanger Centre (<http://www.sanger.ac.uk/>). Referring to a known N-terminal sequence of KS1 strain GDH β subunit (SEQ ID No: 9), there was designed an amino acid sequence (SEQ ID NO: 10) that has high homology to each cytochrome c subunit of an alcohol dehydrogenase derived from *Acetobacter* Sp. or *Gluconobacter* Sp. (Tamaki T. et al., Biochim Biochys Acta 1088 (2): 292-300 (1991), Matsushita K., et al., Biosci. Biotech. Biochem., 56, 304-310 (1992), Takemura H., et al., J Bacteriol, 175, 6857-66 (1993), Kondo K. et al., Appl

Environ Microbiol, 63, 1131-8 (1997)); a gluconate dehydrogenase derived from *Erwinia* sp. or *Pseudomonas* sp. (Yum DY, et al., J Bacteriol, 179, 6566-72 (1997), Matsushita K. et al., J Biochem, 85, 1173-81 (1979)); a sorbitol dehydrogenase derived from *Gluconobacter* sp. (Choi, E.S., et al., FEMS Microbiol. Lett., 125, 45-50 (1995)); and a 2-ketogluconate dehydrogenase derived from *Erwinia* sp. or *Pantoea* sp. (Pujol CJ et al., J Bacteriol, 182, 2230-7, (2000)).

Based on the aforementioned amino acid sequence, gene sequences that encode amino acid sequences having high homologies have been searched from the aforementioned database of *Burkholderia cepacia* J2315 strain by BLAST. Then, the obtained five sequences were searched for homology with the C-terminal sequence of the GDH α subunit of KS1 strain. As a result, amino acid sequences translated from two gene fragments showed high homologies (>90%). Each gene fragment was as short as 200 to 500 bp, so that sequences having high homologies with these sequences were searched from the genome database of *Burkholderia cepacia* J2315 strain by BLAST and the fragments were joined each other. As a result, a fragment of 3,110 bp was obtained. In the obtained nucleotide sequence, there existed an ORF that is presumed to be the C-terminus of the GDH and an ORF that is presumed to be cytochrome C structural gene of 1,275 bp (SEQ ID NO: 11). The amino acid sequence encoded by the ORF is shown in SEQ ID NO: 12. Results of comparison between the obtained nucleotide sequence of the J2315 strain and the nucleotide sequence of the α subunit of KS1 strain that has already been cloned indicate that in the downside of the α subunit,

the nucleotide sequence having a high homology with the nucleotide sequence encoding the signal peptide of cytochrome C of J2315 strain is contained.

From the above, the third ORF in the cloned fragment of *Burkholderia cepacia* KS1 strain obtained in Reference Example 1 (nucleotides 2386 et seq. of SEQ ID NO: 1) is presumed to encode the β subunit. The amino acid sequence at the N-terminus of the purified β subunit corresponds to the 5 amino acid residues translated by the nucleotide sequence consisting of nucleotides 2452 to 2466 in SEQ ID NO: 1, which also suggests that the aforementioned ORF encodes the β subunit.

<2> Amplification of β subunit structural gene using inverse PCR method

(1) Culture of microorganism cell and extraction of genome

Using 5 ml of complete medium (0.5% polypepton, 0.3% yeast extract, 0.5% NaCl), KS1 strain was cultured with shaking at 37°C overnight. Genome was extracted from the obtained microorganism cells using GenomicPrep™ Cells and Tissue DNA Isolation Kit (Amersham Pharmacia Biotech). The method was performed in accordance with the attached manual. The obtained genome was subjected to phenol/chloroform treatment and precipitated with ethanol, and then dissolved in purified water.

(2) Cyclization of genome fragment

The genome extracted from the KS1 strain was digested with *Bam*HI, *Eco*RI, *Hind*III, *Sma*I, *Sac*I, and *Xho*I and the genome fragments were recovered by precipitation with ethanol. Then, 1 μ g of genome digested with the restriction enzymes was subjected to ligation reaction using a DNA

ligation kit (Takara Shuzo Co., Ltd.) at 16°C overnight.

(3) PCR

50 pmol of forward primer (EF1 SEQ ID NO: 13) designed based on the nucleotide sequence in the N-terminal signal sequence region of the GDH β subunit of the KS1 strain, 50 pmol of reverse primer (ER1 SEQ ID NO: 14) (all the primers were synthesized by Invitrogen on consignment), 0.5 ml of LATaq (Takara Bio Co., Ltd.), 8 μ l of dNTP solution, and 5 μ l of 10 \times PCR buffer was added to purified water so as to have a total volume of 50 μ l, and PCR was performed using a program temp control system PC-801 (ASTEC). The PCR reaction was performed under the following conditions: after 30 cycles of 94°C for 5 minutes, 98°C for 20 seconds, 62°C for 30 seconds, 72°C for 6 minutes, and 72°C for 10 minutes.

When the genome digested with a restriction enzyme (*Sma*I) is used as a template, a fragment having a size of about 2.1 kbp was confirmed on Agarose electrophoresis.

<3> Sequencing of PCR-amplified fragment

(1) TA cloning

After the aforementioned inverse PCR product was electrophoresed on Agarose gel, the band was cut out and purified using Gene clean II KIT (Bio101 inc.). The fragment was ligated to pGEM-T Vector using pGEMR-T and pGEMR-T EASY Vector Systems (Promega). *E. coli* DH5 α was transformed with the ligated vector, and the transformant was cultured on an L-agar medium containing 50 μ g/ml ampicillin, 40 μ g/ml X-Gal, and 0.1 μ M IPTG overnight. From the appeared colonies, white colonies were selected and cultured in an L medium containing 50 μ g/ml ampicillin overnight, followed by extraction of plasmids from the cells by the alkali method.

(2) Preparation of sequence sample

The obtained plasmid was treated with RNase and 0.6 volume of 20% PEG6000/2.5 M NaCl was added thereto. The mixture was left to stand on ice for 1 hour. Thereafter, the mixture was centrifuged at 15,000 rpm and 4°C for 15 minutes to obtain a pellet. The pellet was washed with 70% ethanol and dried in vacuum. The dried product was dissolved in purified water.

(3) Analysis of nucleotide sequence of DNA

The nucleotide sequence of the inserted fragment of the plasmid obtained in (2) was analyzed using ABI PRISM™ 310 Genetic Analyzer (PERKIN-ELMER Applied Biosystems). A portion of the sequence of the inserted fragment was determined from the multicloning site of the vector using M13 primer. As a result, the nucleotide sequence containing the N-terminus of the β subunit that had been already analyzed was confirmed. Based on this sequence, primers were sequentially prepared and used to determine the nucleotide sequence of the inserted fragment. The result is shown in SEQ ID NO: 15. Further, the amino acid sequence encoded by the ORF in the nucleotide sequence is shown in SEQ ID NO: 16.

The β subunit has 425 amino acid residues in total, and from the comparison with the N-terminal amino acid sequence already obtained, 22 residues among them are considered to be a signal peptide. The molecular weight of the β subunit calculated based on the amino acid sequence is 45,276 Da and the molecular weight 42,731 Da of the portion excluding the signal peptide is substantially identical to the molecular weight 43 kDa of the GDH β subunit of the KS1 strain. In the amino acid sequence of the β subunit, linking motifs (SEQ ID

NO: 18) that links with hem in cytochrome C were confirmed at 3 positions. The ORFs were located immediately downstream of the ORF of the structural gene of the α subunit, and a sequence that is presumed to be an SD sequence existed upstream of the initiation codon.

Homology search for the obtained amino acid sequence by BLAST showed overall high homologies; a 65% homology with cytochrome C subunit of oxidoreductase dehydrogenase derived from *Ralstonia solanacearum*, a 48% homology with a cytochrome C subunit of sorbitol dehydrogenase derived from *Gluconobacter oxydans*, a 44% homology with a cytochrome C subunit of gluconic acid dehydrogenase derived from *Eriwinia cypripedii*, and a 46.4% homology on an amino acid level with a cytochrome C subunit of 2-keto-gluconic acid dehydrogenase derived from *Pantoea citrea*. Furthermore, the amino acid sequences of cytochromes C reserved a hem-linking motif (SEQ ID NO: 18).

The structural gene of the GDH β subunit of the KS1 strain has a homology of 92.0% on the nucleotide sequence level and of 92.2% on an amino acid level with the structural gene of the GDH β subunit of the J2315 strain.
[Effect of the Invention]

The present invention provides the GDH β subunit of a microorganism belonging to the genus *Burkholderia* and the DNA encoding it.

SEQUENCE LISTING

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<130> P-9842

<141> 2002-04-26

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cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa    338

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Gly	Ala	Leu	Ala	Leu	Thr	Ala	Ala	Gly	Leu	Thr	Gly	Ser	Leu	Thr	Leu	
			30					35				40				
cgg	gcg	ctt	gca	gac	aac	ccc	ggc	act	gcg	ccg	ctc	gat	acg	ttc	atg	434
Arg	Ala	Leu	Ala	Asp	Asn	Pro	Gly	Thr	Ala	Pro	Leu	Asp	Thr	Phe	Met	
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〈213〉 *Burkholderia cepacia*

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<213> Burkholderia cepacia

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Gly	Val	Ala	Gly	Ala	Ile	Val	Ala	His	Gln	Leu	Ala	Met	Ala	Gly	Lys
			20					25					30		
Ala	Val	Ile	Leu	Leu	Glu	Ala	Gly	Pro	Arg	Met	Pro	Arg	Trp	Glu	Ile
		35					40					45			
Val	Glu	Arg	Phe	Arg	Asn	Gln	Pro	Asp	Lys	Met	Asp	Phe	Met	Ala	Pro
	50					55					60				
Tyr	Pro	Ser	Ser	Pro	Trp	Ala	Pro	His	Pro	Glu	Tyr	Gly	Pro	Pro	Asn
65					70					75				80	
Asp	Tyr	Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile
			85						90					95	
Arg	Ala	Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg
			100					105					110		
Phe	Ile	Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg
		115					120					125			
Asp	Trp	Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala
	130					135					140				
Glu	Glu	Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr
145				150					155					160	
Ser	Pro	Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe
			165					170					175		
Asn	Glu	Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe
		180						185					190		
His	Val	Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly
		195					200					205			
Arg	Pro	Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile
	210					215				220					
Gly	Ala	Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala
225				230						235				240	
Gly	Ala	Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly
			245						250					255	

Pro Asp Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala
 260 265 270
 Glu His Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile
 275 280 285
 Glu Thr Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn
 290 295 300
 Gly Val Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His
 305 310 315 320
 Pro Gly Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly
 325 330 335
 Arg Gly Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro
 340 345 350
 Phe Arg Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser
 355 360 365
 Arg Ile Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met
 370 375 380
 Lys Pro Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr
 385 390 395 400
 Val Gln Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg
 405 410 415
 Ile Val Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro
 420 425 430
 Glu Ile Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His
 435 440 445
 Thr Arg Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp
 450 455 460
 Val Val Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser
 465 470 475 480
 Thr Ile Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys
 485 490 495
 Arg Thr Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met
 500 505 510
 Pro Thr Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala
 515 520 525
 Leu Arg Met Ser Asp Thr Leu Lys Lys Glu Val
 530 535

<210> 4

<211> 27

<212> PRT

<213> Burkholderia cepacia

<400> 4

Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu

1

5

10

15

Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp

20

25

<210> 5

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

cccaagcttg ggccgatacc gatacgca

28

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

gagaagcttt ccgcacggtc agacttcc

29

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 7

catgccatgg cacacaacga caacact

27

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

cccaagcttg ggcagactt ccttcttcag c

31

<210> 9

<211> 16

<212> PRT

<213> Burkholderia cepacia

<400> 9

Ala Asp Ala Ala Asp Pro Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala

1

5

10

15

<210> 10

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus

<220>

<221> UNSURE

<222> (6, 17, 18, 19, 22)

<223> Xaa=unknown

<400> 10

Ala Asp Ala Ala Asp Xaa Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala

1

5

10

15

Xaa Xaa Xaa Asp Cys Xaa Ala Cys His

20

25

<210> 11

<211> 2410

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (673)..(1950)

<400> 11

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cgccccgcag gatatgacgt cgctgacggt tticcgcgac ggcccggtcc gcgcgaccga 120
agccgcgaag aagatccatc tgtcgaacat gtcccgcatc aaccaggaga cgcagaagat 180
cttcaaggcc ggcaaactga tgaagcacga ggagctcgac gcgcagatcc gcgaccgttc 240
cgcgcgctac gtgcagttcg actgtctcca cgagattctg ccgcagcccc agaaccgcat 300
cgtgccgagc aagacggcca ccgacgcgat cgggatcccc cgccccgaga tcacgtatgc 360
gatcgacgat tacgtgaagc gcggcgccgt gcacacgcgc gaggcttacg cgacggccgc 420
gaaggtgtcg ggcggcaccg acgtcgtctt caacgacgag ttcgcgccga acaaccacat 480
cacgggcgcg aggatcatgg gcgcggatgc acgcgactcg gtcgtcgaca aggactgccg 540
cacgttcgac catccgaacc tgttctcttc gagcagctcg acgatgccga ccgtcgggtac 600
ggatgaacgtg acgtcgacga tcgcggcgct cgcgctcgcg atgtcggaca cgctgaagaa 660
ggaagtctga cc gtg cgg aaa tct act ctc acc ttc ctc ctc gcc ggc tgc 711
      Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys
            1             5             10
ctc gcg ctg ccc ggc ctc gca cgc gcg gcc gat tgc gcc gat ccg gcg 759
Leu Ala Leu Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala
      15             20             25
cat gtc aag cgc ggc gaa tac ctc gcc gtc gcg ggc gac tgc atg gca 807
His Val Lys Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala
      30             35             40             45
tgc cac acc gcg aag ggc ggc aag ccg ttc gcg ggc ggc ctc ggc atg 855
Cys His Thr Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met
            50             55             60
ccg gtg ccg atg ctc ggc aag atc tat acg agc aac atc aca ccg gat 903
Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp
            65             70             75
ccc gat acc ggc atc ggc aac tgg acg ttc gag gac ttc gag cgc gcg 951
Pro Asp Thr Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala
            80             85             90
gtg cgg cac ggc gta tgc aag aac ggc gac aac ctg tac ccg gcg atg 999
Val Arg His Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met
            95             100             105
ccg tac gtg tgc tac gcg aag atc aac gac gac gac gtg caa gcg ctg 1047
Pro Tyr Val Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu

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110	115	120	125	
tac gcg tac ttc atg cac ggc gtc gaa ccg gtc aag cag gcg ccg ccg				1095
Tyr Ala Tyr Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro				
	130	135	140	
aag aac gag atc ccc gcg ctg ctg agc atg cgc tgg ccg ctg aag atc				1143
Lys Asn Glu Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile				
	145	150	155	
tgg aac tgg ctg ttc ctg aag gac ggc gtg tac cag ccg aag ccc gag				1191
Trp Asn Trp Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu				
	160	165	170	
cag agc gcc gag tgg aac cgc ggc gcc tat ctc gtg cag ggc ctc gcg				1239
Gln Ser Ala Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala				
	175	180	185	
cac tgc agc acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag				1287
His Cys Ser Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys				
	190	195	200	205
tcg ctc gac gaa acg ggc ggc agc ttc ctg tcg ggc tcg gtg ctc gcg				1335
Ser Leu Asp Glu Thr Gly Gly Ser Phe Leu Ser Gly Ser Val Leu Ala				
	210	215	220	
ggc tgg gac ggc tac aac atc acg tcc gac ccg aac gcg ggg atc ggc				1383
Gly Trp Asp Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly				
	225	230	235	
ggc tgg acg cag cag cag ctc gtc cag tac ctg cgc acc ggc agc gtg				1431
Gly Trp Thr Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val				
	240	245	250	
ccg ggc ctc gcg cag gcg gcc ggc ccg atg gcc gag gcg atc gag cac				1479
Pro Gly Leu Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Ile Glu His				
	255	260	265	
agc ttc tcg aag atg acc gaa gcc gac atc ggc ggc ccg atg gcc gag				1527
Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Gly Pro Met Ala Glu				
	270	275	280	285
gcg atc gag cac agc ttc tcg aag atg acc gaa gcc gac atc ggc cgc				1575
Ala Ile Glu His Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Arg				
	290	295	300	
tcg tcg tgg ggc aag ccg gcc gag gat ggc ctg aag ctg cgc ggc gtc				1623
Ser Ser Trp Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val				
	305	310	315	
gcg ctc gcg tcg tcg ggc atc gat ccg gca ccg ctg tat ctc ggc aac				1671
Ala Leu Ala Ser Ser Gly Ile Asp Pro Ala Pro Leu Tyr Leu Gly Asn				
	320	325	330	
tgc gcg acc tgc cac cag atg cag ggc aag ggc acg ccg gac ggt tac				1719

Cys Ala Thr Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr
 335 340 345
 tac ccg ccg ttg ttc cac aac tcg acg gtc ggc gcg tcg aat ccg acc 1767
 Tyr Pro Pro Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Thr
 350 355 360 365
 aac ctc gtg cag gtg atc ctg aac ggc gtg cag cgc aag gcc ggc agc 1815
 Asn Leu Val Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ala Gly Ser
 370 375 380
 gag gac gtc ggg atg ccc gcg ttc cgc cac gag ctg tcg gat gcg cag 1863
 Glu Asp Val Gly Met Pro Ala Phe Arg His Glu Leu Ser Asp Ala Gln
 385 390 395
 atc gcc gcg ctg acg aac tac ctg acg ggc cag ttc ggc aat ccg gcc 1911
 Ile Ala Ala Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala
 400 405 410
 gcg aag gtg acc gag cag gac gtc gcg aag ctg cgc tga aacgcggcac 1960
 Ala Lys Val Thr Glu Gln Asp Val Ala Lys Leu Arg
 415 420 425
 gcggcgaggc agggcaacaa tagaaaagag gaggagcaca gcacatcggg cgggccccga 2020
 tgccggttgt tgcagagcgg gacgggcggc gcaggcggtc gcccgtcctg gttcacaggc 2080
 aatccggtgc gcgcacgccg cgcacgtgtt tcgttgatcg agaccatgac accgaaccaa 2140
 ccgtttctcg cgtcccagcg cgtatgtgtg ctgctgtgtt cccgaatcct gctcgtgatc 2200
 ctgttcgtga tgttcggctg gaagaagatt atcgacttct ccggtacgat cgcgttcgatg 2260
 ggcagcgagg gcgcgccggc gccgatcctc tcggcggcga tctccgtcgt gatggagctc 2320
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 ctgtacacga tcggtaccgg catcatcggc 2410

<210> 12

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 12

Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys Leu Ala Leu
 1 5 10 15
 Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala His Val Lys
 20 25 30
 Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala Cys His Thr
 35 40 45
 Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met Pro Val Pro
 50 55 60
 Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr

65		70		75		80									
Gly	Ile	Gly	Asn	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His
		85							90					95	
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val
		100						105					110		
Ser	Tyr	Ala	Lys	Ile	Asn	Asp	Asp	Asp	Val	Gln	Ala	Leu	Tyr	Ala	Tyr
		115						120					125		
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu
		130						135					140		
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp
145							150				155				160
Leu	Phe	Leu	Lys	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Pro	Glu	Gln	Ser	Ala
				165						170				175	
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser
			180						185					190	
Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp
		195						200					205		
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp
		210						215					220		
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Gly	Trp	Thr
225						230					235				240
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Leu
				245						250				255	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His	Ser	Phe	Ser
			260						265				270		
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu
		275						280				285			
His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg	Ser	Ser	Trp
		290					295					300			
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305						310					315				320
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
				325						330				335	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Pro
			340						345				350		
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr	Asn	Leu	Val
		355						360					365		
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser	Glu	Asp	Val
		370						375				380			
Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln	Ile	Ala	Ala
385						390					395				400

Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala Ala Lys Val
405 410 415
Thr Glu Gln Asp Val Ala Lys Leu Arg
420 425

<210> 13
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
tgcaccgtgc ggaaatctac tctcact 27

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
acttcttctt tcagcgtgtc cgacatc 27

<210> 15
 <211> 1441
 <212> DNA
 <213> Burkholderia cepacia

$\langle 220 \rangle$
 $\langle 221 \rangle$ CDS
 $\langle 222 \rangle$ (121) .. (1398)

<400> 15
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gctgacgata gccgcgctcg cgctgcggat gtcggacacg ctgaagaagg aagtcctgacc 120
gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu

1	5	10	15	
ccg ggc ttc gcg cgc gcg gcc gat gcg gcc gat ccg gcg ctg gtc aag				216
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys				
20	25	30		
cgc ggc gaa tac ctc gcg acc gcc atg ccg gta ccg atg ctc ggc aag				264
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys				
35	40	45		
atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg				312
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met				
50	55	60		
gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc				360
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly				
65	70	75	80	
ggc atc ggc aaa tgg acg ttc gag gac ttc gag cgc gcg gtg cgg cac				408
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His				
85	90	95		
ggc gtg tgc aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg				456
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val				
100	105	110		
tcg tac gcg aag atc aag gac gac gac gta cgc gcg ctg tac gcc tac				504
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr				
115	120	125		
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg ccg aag aac gag				552
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu				
130	135	140		
atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg				600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp				
145	150	155	160	
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc				648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala				
165	170	175		
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc				696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser				
180	185	190		
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac				744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp				
195	200	205		
gaa acc ggc ggc agc ttc ctc gcg ggg tcg gtg ctc gcc ggc tgg gac				792
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp				
210	215	220		
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg				840

Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Ser	Trp	Thr	
225					230					235					240	
cag	cag	cag	ctc	gtg	cag	tat	tig	cgc	acc	ggc	agc	gtg	ccg	ggc	gtc	888
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val	
				245						250					255	
gcg	cag	gcg	gcc	ggg	ccg	atg	gcc	gag	gcg	gtc	gag	cac	agc	ttc	tcg	936
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser	
				260						265					270	
aag	atg	acc	gaa	gcg	gac	atc	ggt	gcg	atc	gcc	acg	tac	gtc	cgc	acg	984
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr	
				275						280					285	
gtg	ccg	gcc	gtt	gcc	gac	agc	aac	gcg	aag	cag	ccg	cgg	tcg	tcg	tgg	1032
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp	
				290						295					300	
ggc	aag	ccg	gcc	gag	gac	ggg	ctg	aag	ctg	cgc	ggt	gtc	gcg	ctc	gcg	1080
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala	
305					310					315					320	
tcg	tcg	ggc	atc	gat	ccg	gcg	cgg	ctg	tat	ctc	ggc	aac	tgc	gcg	acg	1128
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr	
				325						330					335	
tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggc	tat	tac	ccg	tcg	1176
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser	
				340						345					350	
ctg	ttc	cac	aac	tcc	acc	gtc	ggc	gcg	tcg	aat	ccg	tcg	aac	ctc	gtg	1224
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val	
				355						360					365	
cag	gtg	atc	ctg	aac	ggc	gtg	cag	cgc	aag	atc	ggc	agc	gag	gat	atc	1272
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile	
				370						375					380	
ggg	atg	ccc	gct	ttc	cgc	tac	gat	ctg	aac	gac	gcg	cag	atc	gcc	gcg	1320
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala	
385					390					395					400	
ctg	acg	aac	tac	gtg	acc	gcg	cag	ttc	ggc	aat	ccg	gcg	gcg	aag	gtg	1368
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val	
				405						410					415	
acg	gag	cag	gac	gtc	gcg	aag	ctg	cgc	tga	catagtcggg	cgcgccgaca					1418
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg								
				420						425						
cggcgcgaacc	gataggacag gag															1441

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 16

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Arg	Gly	Glu	Tyr	Leu	Ala	Thr	Ala	Met	Pro	Val	Pro	Met	Leu	Gly	Lys
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Ala	Cys	His	Thr	Val	Lys	Gly	Gly	Lys	Pro	Tyr	Ala	Gly	Gly	Leu	Gly
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Gly	Ile	Gly	Lys	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His
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Ser	Tyr	Ala	Lys	Ile	Lys	Asp	Asp	Asp	Val	Arg	Ala	Leu	Tyr	Ala	Tyr
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Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu
	130					135					140				
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp
	145				150				155					160	
Leu	Phe	Leu	Lys	Asp	Gly	Pro	Tyr	Gln	Pro	Lys	Pro	Ser	Gln	Ser	Ala
			165					170					175		
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser
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Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp
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Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val
			245					250					255		
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser
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Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr
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Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp
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Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
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Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
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Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser
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Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile
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Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: heme binding motif

<220>

<221> UNSURE

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<400> 17

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<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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27

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

cccaagcttg ggtcagactt ccttcttcag c

31

[Name of the Document] Abstract

[Abstract]

[Object] It is to provide a DNA encoding a GDH β subunit of a microorganism belonging to the genus *Burkholderia* and a method of using the DNA.

[Solving Means] A DNA fragment encoding a β subunit is obtained by inverse PCR using primers designed based on the nucleotide sequence of a N-terminal signal sequence region of a GDH β subunit derived from *Burkholderia cepacia* KS1 strain.

[Drawing selected] None